Ref #	Hits	Search Query	DBs	Default Operator	Plurals	Time Stamp
L1	219	(magnetic or magnetism or magnetization) near10 (spatial or orientation) near15 (DNA or RNA or protein or peptide or analyte or target)	USPAT; EPO; JPO; DERWENT	OR	OFF	2006/02/02 17:07
L2	83	l1 same (detect$ or determ$ or measur$)	USPAT; EPO; JPO; DERWENT	OR	OFF	2006/02/02 16:35
L3	38	l2 and @py<"2002"	USPAT; EPO; JPO; DERWENT	OR	OFF	2006/02/02 16:36
L4	11	(magnetic or magnetism or magnetization) near10 (spatial or orientation) near15 (DNA or RNA or protein or peptide or analyte)	USPAT; EPO; JPO; DERWENT	OR	OFF	2006/02/02 16:41
L5	253	(magnetic or magnetism or magnetization) same (spatial or orientation) same (DNA or RNA or protein or peptide or analyte)	USPAT; EPO; JPO; DERWENT	OR	OFF	2006/02/02 16:42
L6	227	(magnetic or magnetism or magnetization) same (spatial or orientation) same (DNA or RNA or protein or peptide)	USPAT; EPO; JPO; DERWENT	OR	OFF	2006/02/02 16:42
L7	164	(magnetic or magnetism or magnetization) same (spatial or orientation) same (DNA or RNA or protein or peptide) same (detect$ or measur$ or determin$)	USPAT; EPO; JPO; DERWENT	OR	OFF	2006/02/02 16:52
L8	53	l7 and @py<"2002"	USPAT; EPO; JPO; DERWENT	OR	OFF	2006/02/02 16:43
L9	63	(magnetic or magnetism or magnetization) near8 (spatial or orient$) near10 (DNA or RNA or protein or peptide or analyte or target) near10 (detect$ or measur$ or determin$)	USPAT; EPO; JPO; DERWENT	OR	OFF	2006/02/02 16:53
L10	40	l9 and @py<"2003"	USPAT; EPO; JPO; DERWENT	OR	OFF	2006/02/02 16:53
L11	2	(magnetic or magnetism or magnetization) near10 (spatial near2 orientation) near15 (DNA or RNA or protein or peptide or analyte or target)	USPAT; EPO; JPO; DERWENT	OR	OFF	2006/02/02 17:08

Ref #	Hits	Search Query	DBs	Default Operator	Plurals	Time Stamp
L1	1874	(hysteresis near2 loop) same magnet$	USPAT; EPO	OR	OFF	2006/02/02 13:31
L2	317	(hysteresis near2 loop).CLM.	USPAT; EPO	OR	OFF	2006/02/02 13:31
L3	185	l1 and l2	USPAT; EPO	OR	OFF	2006/02/02 13:31
L4	0	l3 and analyte	USPAT; EPO	OR	OFF	2006/02/02 13:31
L5	125	l3 and signal	USPAT; EPO	OR	OFF	2006/02/02 13:31
L6	63	l3 and (signal same hysteresis)	USPAT; EPO	OR	OFF	2006/02/02 13:32
L7	0	l6 and biological	USPAT; EPO	OR	OFF	2006/02/02 13:32
L8	0	l6 and (protein or peptide or DNA or nucleic or antibody or antigen)	USPAT; EPO	OR	OFF	2006/02/02 13:32
L9	5	l6 and target	USPAT; EPO	OR	OFF	2006/02/02 13:34
L10	3	l6 and probe	USPAT; EPO	OR	OFF	2006/02/02 13:34

NEWS 3 DEC 05 CASREACT(R) - Over 10 million reactions available
NEWS 4 DEC 14 2006 MeSH terms loaded in MEDLINE/LMEDLINE
NEWS 5 DEC 14 2006 MeSH terms loaded for MEDLINE file segment of TOXCENTER
NEWS 6 DEC 14 CA/CAplus to be enhanced with updated IPC codes
NEWS 7 DEC 21 IPC search and display fields enhanced in CA/CAplus with the IPC reform
NEWS 8 DEC 23 New IPC8 SEARCH, DISPLAY, and SELECT fields in USPATFULL/ USPAT2
NEWS 9 JAN 13 IPC 8 searching in IFIPAT, IFIUDB, and IFICDB
NEWS 10 JAN 13 New IPC 8 SEARCH, DISPLAY, and SELECT enhancements added to INPADOC
NEWS 11 JAN 17 Pre-1988 INPI data added to MARPAT
NEWS 12 JAN 17 IPC 8 in the WPI family of databases including WPIFV
NEWS 13 JAN 30 Saved answer limit increased
NEWS 14 JAN 31 Monthly current-awareness alert (SDI) frequency added to TULSA

NEWS EXPRESS JANUARY 03 CURRENT VERSION FOR WINDOWS IS V8.01, CURRENT MACINTOSH VERSION IS V6.0c(ENG) AND V6.0Jc(JP), AND CURRENT DISCOVER FILE IS DATED 19 DECEMBER 2005. V8.0 USERS CAN OBTAIN THE UPGRADE TO V8.01 AT http://download.cas.org/express/v8.0-Discover/

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NEWS PHONE Direct Dial and Telecommunication Network Access to STN
NEWS WWW CAS World Wide Web Site (general information)

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FILE 'HOME' ENTERED AT 17:09:59 ON 02 FEB 2006

=> file .meeting

'EVENTLINE' IS NOT A VALID FILE NAME
Enter "HELP FILE NAMES" at an arrow prompt (=>) for a list of files
that are available. If you have requested multiple files, you can
specify a corrected file name or you can enter "IGNORE" to continue
accessing the remaining file names entered.
ENTER A FILE NAME OR (IGNORE):ignore
'MEDICONF' IS NOT A VALID FILE NAME
Enter "HELP FILE NAMES" at an arrow prompt (=>) for a list of files
that are available. If you have requested multiple files, you can
specify a corrected file name or you can enter "IGNORE" to continue
accessing the remaining file names entered.
ENTER A FILE NAME OR (IGNORE):ignore

COST IN U.S. DOLLARS	SINCE FILE ENTRY	TOTAL SESSION
FULL ESTIMATED COST	0.21	0.21

FILE 'AGRICOLA' ENTERED AT 17:10:44 ON 02 FEB 2006

FILE 'BIOTECHNO' ENTERED AT 17:10:44 ON 02 FEB 2006

FILE 'CONFSCI' ENTERED AT 17:10:44 ON 02 FEB 2006

FILE 'HEALSAFE' ENTERED AT 17:10:44 ON 02 FEB 2006

FILE 'IMSDRUGCONF' ENTERED AT 17:10:44 ON 02 FEB 2006

FILE 'LIFESCI' ENTERED AT 17:10:44 ON 02 FEB 2006

FILE 'PASCAL' ENTERED AT 17:10:44 ON 02 FEB 2006

=> (spatial orientation) and (magnetic or magnetization or magnetism) and (bind or bound)

L1	0 FILE AGRICOLA
L2	4 FILE BIOTECHNO
L3	0 FILE CONFSCI
L4	0 FILE HEALSAFE
L5	0 FILE IMSDRUGCONF

L6 1 FILE LIFESCI
L7 1 FILE PASCAL

TOTAL FOR ALL FILES
L8 6 (SPATIAL ORIENTATION) AND (MAGNETIC OR MAGNETIZATION OR MAGNETIS
M) AND (BIND OR BOUND)

=> dup rem
ENTER L# LIST OR (END):l8
DUPLICATE IS NOT AVAILABLE IN 'IMSDRUGCONF'.
ANSWERS FROM THESE FILES WILL BE CONSIDERED UNIQUE
PROCESSING COMPLETED FOR L8
L9 5 DUP REM L8 (1 DUPLICATE REMOVED)

=> d l9 ibib abs total

L9 ANSWER 1 OF 5 BIOTECHNO COPYRIGHT 2006 Elsevier Science B.V. on STN
ACCESSION NUMBER: 2003:36315140 BIOTECHNO
TITLE: The three-dimensional structural surface of two .beta.-sheet scorpion toxins mimics that of an .alpha.-helical dihydropyridine receptor segment
AUTHOR: Green D.; Pace S.; Curtis S.M.; Sakowska M.; Lamb G.D.; Dulhunty A.F.; Casarotto M.G.
CORPORATE SOURCE: M.G. Casarotto, Division of Molecular Bioscience, John Curtin Sch. of Medical Research, Australian National University, P.O. Box 334, Canberra, ACT 2601, Australia.
E-mail: Marco.Casarotto@anu.edu.au
SOURCE: Biochemical Journal, (01 MAR 2003), 370/2 (517-527), 34 reference(s)
CODEN: BIJOAK ISSN: 0264-6021
DOCUMENT TYPE: Journal; Article
COUNTRY: United Kingdom
LANGUAGE: English
SUMMARY LANGUAGE: English
AN 2003:36315140 BIOTECHNO
AB An .alpha.-helical II-III loop segment of the dihydropyridine receptor activates the ryanodine receptor calcium-release channel. We describe a novel manipulation in which this agonist's activity is increased by modifying its surface structure to resemble that of a toxin molecule. In a unique system, native .beta.-sheet scorpion toxins have been reported to activate skeletal muscle ryanodine receptor calcium channels with high affinity by binding to the same site as the lower-affinity .alpha.-helical dihydropyridine receptor segment. We increased the

alignment of basic residues in the .alpha.-helical peptide to mimic the spatial orientation of active residues in the scorpion toxin, with a consequent 2-20-fold increase in the activity of the .alpha.-helical peptide. We hypothesized that, like the native peptide, the modified peptide and the scorpion toxin may bind to a common site. This was supported by (i) similar changes in ryanodine receptor channel gating induced by the native or modified .alpha.-helical peptide and the .beta.-sheet toxin, a 10-100-fold reduction in channel closed time, with a <=2-fold increase in open dwell time and (ii) a failure of the toxin to further activate channels activated by the peptides. These results suggest that diverse structural scaffolds can present similar conformational surface properties to target common receptor sites.

L9 ANSWER 2 OF 5 BIOTECHNO COPYRIGHT 2006 Elsevier Science B.V. on STN

DUPLICATE

ACCESSION NUMBER: 2002:34679602 BIOTECHNO

TITLE: Polyamine-nucleic acid interactions and the effects on structure in oriented DNA fibers

AUTHOR: van Dam L.; Korolev N.; Nordenskiold L.

CORPORATE SOURCE: L. Nordenskiold, Arrhenius Laboratory, Stockholm University, S-106 91 Stockholm, Sweden.
E-mail: lnor@physc.su.se

SOURCE: Nucleic Acids Research, (15 JAN 2002), 30/2 (419-428), 60 reference(s)
CODEN: NARHAD ISSN: 0305-1048

DOCUMENT TYPE: Journal; Article

COUNTRY: United Kingdom

LANGUAGE: English

SUMMARY LANGUAGE: English

AN 2002:34679602 BIOTECHNO

AB Fibrous oriented calf thymus DNA containing the natural polyamines spermidine (Spd) and putrescine (Put), and the degradation polyamines cadaverine (Cad) and 1,3-diaminopropane (DAP), have been investigated at different water contents using nuclear magnetic resonance (NMR) methods, fiber X-ray diffraction and gravimetric measurements. When judged by X-ray only the DAP and Spd samples seem to undergo a B-A-form transition at reduced water activity. Solid-state two-dimensional rotor-synchronized magic angle spinning (2D-syncMAS) .sup.3.sup.1P-NMR, however, shows the A-form to be present also in the Put sample, and it appears that the separation between the amine units of diamines is correlated with the amount of A-form present. In addition, the solid-state NMR data show the polyamine-bound DNA samples to have a significant deviation from the ordinary B-form DNA structure, displaying similar amounts of BI and BII nucleotide conformations. The

low water content of the samples suggest that the polyamines themselves act as hydrators of DNA. Water .sup.2H-NMR results are in agreement with this observation. The quadrupolar splittings of the polyamine .sup.2H signals for samples at low water content indicate some preferential spatial orientations of the polyamines in the ordered DNA environment. The polyamines show relatively fast macroscopic diffusion as detected by NMR self-diffusion measurements.

L9 ANSWER 3 OF 5 PASCAL COPYRIGHT 2006 INIST-CNRS. ALL RIGHTS RESERVED. on STN

ACCESSION NUMBER: 2002-0456282 PASCAL

TITLE (IN ENGLISH): Characterization of the normal cardiac myofiber field in goat measured with MR-diffusion tensor imaging

AUTHOR: GEERTS L.; BOVENDEERD P.; NICOLAY K.; ARTS T.

CORPORATE SOURCE: Department of Mechanical Engineering, Eindhoven University of Technology, 5600 MB Eindhoven, Netherlands; Department of Biomedical Engineering, Eindhoven University of Technology, 5600 MB Eindhoven, Netherlands; Department of Experimental In Vivo NMR, Utrecht University, 3508 TC Utrecht, Netherlands; Department of Biophysics, Maastricht Univesity, Maastricht, 6200 MD, Netherlands

SOURCE: American journal of physiology. Heart and circulatory physiology, (2002), 52(1), H139-H145, 28 refs. ISSN: 0363-6135 CODEN: AJPPDI

DOCUMENT TYPE: Journal

BIBLIOGRAPHIC LEVEL: Analytic

COUNTRY: United States

LANGUAGE: English

AVAILABILITY: INIST-670D, 354000108741710170

AN 2002-0456282 PASCAL

AB Cardiac myofiber orientation is a crucial determinant of the distribution of myocardial wall stress. Myofiber orientation is commonly quantified by helix and transverse angles. Accuracy of reported helix angles is limited. Reported transverse angle data are incomplete. We measured cardiac myofiber orientation postmortem in five healthy goat hearts using magnetic resonance-diffusion tensor imaging. A novel local wall-bound coordinate system was derived from the characteristics of the fiber field. The transmural course of the helix angle corresponded to data reported in literature. The mean midwall transverse angle ranged from -12 .+-. 4.degree. near the apex to +9.0 .+-. 4.degree. near the base of the left ventricle, which is in agreement with the course

predicted by Rijcken et al. (18) using a uniform load hypothesis. The divergence of the myofiber field was computed, which is a measure for the extent to which wall stress is transmitted through the myofiber alone. It appeared to be <0.07 mm.sup.-.sup.1 throughout the myocardial walls except for the fusion sites between the left and right ventricles and the insertion sites of the papillary muscles.

L9 ANSWER 4 OF 5 BIOTECHNO COPYRIGHT 2006 Elsevier Science B.V. on STN

ACCESSION NUMBER: 2001:32221147 BIOTECHNO

TITLE: Solution structure of the DNA-binding domain of the TyrR protein of Haemophilus influenzae

AUTHOR: Wang Y.; Zhao S.; Somerville R.L.; Jardetzky O.

CORPORATE SOURCE: Dr. O. Jardetzky, Department of Molecular Pharmacology, Stanford University, Stanford, CA 94305-5174, United States.
E-mail: jardetzky@stanford.edu

SOURCE: Protein Science, (2001), 10/3 (592-598), 34 reference(s)
CODEN: PRCIEI ISSN: 0961-8368

DOCUMENT TYPE: Journal; Article

COUNTRY: United States

LANGUAGE: English

SUMMARY LANGUAGE: English

AN 2001:32221147 BIOTECHNO

AB The TyrR protein of Haemophilus influenzae is a 36-kD transcription factor whose major function is to control the expression of genes important in the biosynthesis and transport of aromatic amino acids. Using .sup.1H and .sup.1.sup.5N NMR spectroscopy, we have determined the 3D solution structure of the TyrR C-terminal DNA-binding domain (DBD) containing residues from 258 to 318 (TyrR[258-318]). The NMR results show that this segment of TyrR consists of a potential hinge helix at its N terminus (residues 263-270) as well as three well-defined .alpha.-helices extending from residues 277-289 (HR-2), 293-300 (HR-l), and 304-314 (HR). Helix HR-1 and HR fold in a typical helix-turn-helix (HTH) motif. The three helices and the hinge helix are tightly bound together by hydrophobic interaction and hydrogen bonds. Several hydrophilic residues whose side chains may directly interact with DNA are identified. A hydrophobic patch that may be part of the interaction surface between the domains of TyrR protein is also observed. Comparisons with the structures of other HTH DNA-binding proteins reveal that in terms of the spatial orientation of the three helices, this protein most closely resembles the cap family.

L9 ANSWER 5 OF 5 BIOTECHNO COPYRIGHT 2006 Elsevier Science B.V. on STN

ACCESSION NUMBER: 1993:23256982 BIOTECHNO
TITLE: The nuclear magnetic resonance solution structure of flavoridin, an antagonist of the platelet GP IIb-IIIa receptor
AUTHOR: Senn H.; Klaus W.
CORPORATE SOURCE: Dept. of Pharmaceutical Research, New Technol. F. Hoffmann-LaRoche Ltd,CH-4002 Basel, Switzerland.
SOURCE: Journal of Molecular Biology, (1993), 232/3 (907-925)
CODEN: JMOBAK ISSN: 0022-2836
DOCUMENT TYPE: Journal; Article
COUNTRY: United Kingdom
LANGUAGE: English
SUMMARY LANGUAGE: English
AN 1993:23256982 BIOTECHNO
AB The snake venom protein flavoridin, a polypeptide of 70 amino acid residues, is a potent inhibitor of blood platelet aggregation. It binds to cell-surface integrin receptors such as the fibrinogen receptor glycoprotein IIb/IIIa. The inhibitory properties of flavoridin have been attributed to the tripeptide segment Arg-Gly-Asp (residues 49 to 51). This paper describes the determination of the three-dimensional structure of flavoridin in aqueous solution based on two-dimensional nuclear magnetic resonance spectroscopy. A family of 18 conformers was selected to characterize the solution structure. The molecule comprises two structural domains, an N-terminal unit extending from residues 1 to 25, and a C-terminal unit from residues 26 to 70. Whereas the mutual spatial orientation of these regions is not well defined, each one is well organized within itself. The segment 26 to 70, which is homologous to the sequence of the snake toxins echistatin and eristostatin, shows an average value of 1.0 .ANG. for the root-mean-square deviations of the backbone atoms among the 18 conformers The structure of flavoridin consists essentially of non-repetitive elements such as tight turns and loops, whose location and conformation are characterized in this paper. With the exception of two short regions of antiparallel .beta.-sheet, no classic element of protein secondary structure is present. The six disulphide bridges, which have been mapped by applying a novel computational strategy (see accompanying paper), are the dominant organizational feature of the polypeptide fold of flavoridin. Two of the bridges are located in the N-terminal domain, three in the C-terminal domain and one connects the two structural units. The mobile ROD recognition sequence for integrins is located peripheral to the core region of the C-terminal domain at the most exposed end of a nine residue loop structure, which is attached to a short .beta.-sheet. The C terminus is close to this loop structure.